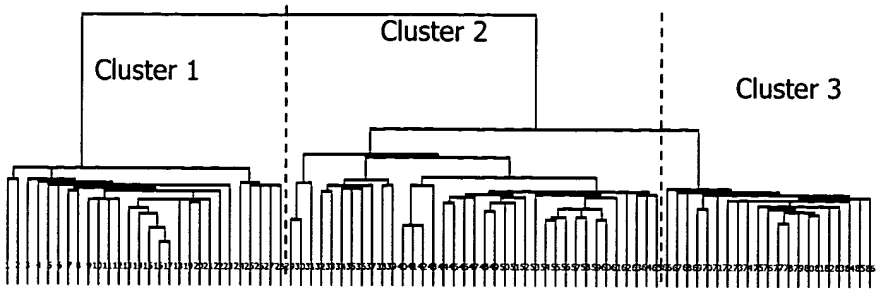
FIGURE 1



	I.D.	Age/Sex	T/N	Stage	Classification	Differentiation	Smoking	Survival	p53	K-ras Codon	K-ras mutation
Cluster 1	1	63.1/F	2/0	1	BD	Moderate	30	20.6	-		
	2	44.6/F	1/0	1	BD	Moderate	15	85.2	-		
	3	51.8/F	1/0	1	BD	Moderate	20	20.2	+		
	4	64/F	3/1	3	BD	Moderate	50	21.2	-	12(1)	G > T
	5	58.8/M	2/2	3	BD	Moderate	48	12.2	not avail	12(1)	G > T
	6	45.8/F	3/1	3	BD	Poor	75	4	+	12(1)	G > T
	7	75.6/F	1/0	1	BD	Moderate	108	36.5	-	12(2)	G > T
	8	54.9/F	1/0	1	B/A	Well	40	1.5	-	12(1)	G > T
	9	76/F	1/0	1	BD	Well	40	63.4	-		
	10	61/F	1/0	1	B/A	Well	100	19.5	-	12(2)	G > C
	11	68.5/F	1/0	1	B/A	Well	5	24.4	-		
	12	84.6/F	1/0	1	B/A	Well	none	30.8	-		
	13	65.6/M	1/0	1	BD	Moderate	90	12.5	+		
	14	63.8/F	1/0	1	BD/PA	Moderate	100	5.8	-		
	15	73.8/M	2/0	1	B/A/MU	Well	55	4.5	-	12(2)	G > A
	16	58.4/M	1/0	1	BA	Well	90	36	-		
	17	74.6/F	1/0	1	BD	Moderate	50	40	-		
	18	75/M	2/0	1	BD	Moderate	14	34.2	-		
	19	67.3/M	1/0	1	BA	Well	30	65.4	-		
	20	79.8/M	2/0	1	BA	Well	30	19.9	-		
	21	72.9/F	1/0	1	B/A	Well	2.5	43.8	-		
	22	46.3/F	1/0	1	B/A / U	Well		40	-		
	23	52.9/F	1/0	1	BD	Poor	60	8.3	+	12(2)	G > C
	24	55.4/M	4/0	3	BD	Poor	50	8.5	-		
	25	62/F	2/0	1	BA/MU	Well	none	30.6	-		
	26	60.2/M	1/0	1	BD/MU	Moderate	60	26.8	-	12(1)	G > T
	27	68.2/F	2/0	1	BD/MU	Moderate	50	10.1	+	12(1)	G > C
	28	49/F	2/0	1	BD	Poor	60	8.7	-		
Cluster 2	29	68.2/F	2/0	1	BA	Well	none	34.7	-	12(2)	G > T
	30	66.2/M	2/0	1	BA	Well		34.6	-	12(2)	G > T
	31	59.4/F	1/0	1	BD	well/mod.	none	13	-	12(2)	G > T
	32	63.7/M	2/2	3	BD/MU	Poor	30	6.1	-		
	33	52.3/F	3/2	3	BD	Moderate	none	52.4	-		
	34	56.5/M	3/2	3	BD	Moderate	40	9.6	-	12(2)	G > C
	35	73.6/F	2/0	1	BD/PA	Moderate	50	54.8	-	12(1)	G > T
	36	62.2/M	2/2	3	BD/PA	Moderate	20	15.1	-	12(1)	G > T
	37	62.1/F	1/0	1	BA/MU	Well	20	25.2	-		
	38	65.4/M	2/0	1	BD	Moderate	12	48.1	+		
	39	58.5/F	2/2	3	BD/PA	Moderate	none	16.6	-		
	40	78.5/F	4/2	3	BD	Poor	2	10	+	12(1)	G > T
	41	62.7/F	1/0	1	B/A	Well	45	10.1	-		
	42	66.8/F	2/0	1	BD	Poor	15	32.2	-		
	43	48.2/F	1/0	1	BD	Moderate	none	98.7	-	12(2)	G > C
	44	60/M	2/0	1	BD	Moderate	27	60.5	-	12(2)	G > A
	45	74.9/F	1/0	1	BD	Poor	30	29.6	-	12(2)	G > A
	46	59.9/F	1/0	1	BD	Moderate	80	107.9	-	12(2)	G > C
	47	63.2/M	1/0	1	BD	Poor	27	39.1	-		
	48	60.4/M	2/0	1	BD	Poor	160	82.4	-	12(1)	G > T
	49	65/M	1/0	1	BD	Moderate	60	84.1	-		
	50	42.8/M	1/0	1	BD	Moderate	60	77.8	-		
	51	67.1/M	1/0	1	BD	Moderate	25	79.5	+	12(2)	G > A
	52	72.1/M	1/0	1	BD/PA	Moderate	100	19	+	13(1)	G > T
	53	66.3/M	1/0	1	BD	Moderate	18	10.4	+		
	54	69.2/F	1/0	1	BA/BD	Well	40	34.1	-		
	55	65.8/F	1/0	1	BD	Moderate	20	70.7	-	12(2)	G > T
	56	56/M	1/0	1	BD	Moderate	80	68.1	+		
	57	63.6/F	1/0	1	B/A	Well	34	4.9	-	12(1)	G > T
	58	82.8/F	1/0	1	B/A	Well	none	25.3	-		
	59	82.5/F	1/0	1	BD	Well	none	48.2	-		
	60	62/F	2/0	1	BA	Well	positive	108.2	-	12(1)	G > T
	61	74.2/F	1/0	1	B/A with PA	Well	75	28.3	-	12(2)	G > T
	62	59.6/M	1/0	1	BD	Moderate	60	52.9	-		
	63	59.5/F	2/0	1	BD	Moderate	positive	93.7	-		
	64	65.6/F	1/0	1	BD	Poor	48	91.8	+		
	65	54.6/F	1/0	1	BD/CC	Moderate	29	110.6	-		

P-VALUES: Differentiation 0.01; Smoking 0.06; p53 0.99; K-ras 0.413; Stage 0.03; BA type 0.006

Note: Smoking=pack years; Survival=Months

Note: Classification: BD=Bronchial Derived; BA=Bronchioloalveolar; PA=Papillary; CC=Clear Cell; MU=Mucinous

* = Deceased

	I.D.	Age/Sex	T/N	Stage	Classification	Differentiation	Smoking	Survival	p53	K-ras Codon	K-ras mutation
Cluster 3	66	76.7/M	2/0	1	BD/CC	Poor	100	47	-		
	67	57.9/F	1/0	1	BD	Poor		91.9	-	12(2)	G > A
	68	51.7/M	2/0	1	BD	Poor	50	45.8	-		
	69	72/F	2/2	3	BD	Poor	50	5.4	-	12(1)	G > T
	70	72/M	3/2	3	BD/MU	Moderate	50	2.4	-		
	71	71.5/F	2/2	3	BD/PA	Moderate	25	54.6	-	12(2)	G > C
	72	46.2/M	1/0	1	BD	Poor	50	87.7	-	13(2)	G > T
	73	54.9/F	1/2	3	BD	Moderate	7.5	20.1	-		
	74	62.6/F	2/0	1	BD	Well	50	14.5	-	12(1)	G > T
	75	84.5/F	1/0	1	BD	Poor	75	1.6	-		
	76	73.1/F	2/0	1	BD/CC	Poor	26	8.4	-	12(1)	G > T
	77	64.4/M	1/2	3	BD	Poor	84	2.6	-	13(2)	G > A
	78	70/M	1/0	1	BD	Poor	60	21.1	+		
	79	69.7/M	1/2	3	BD/PA	Moderate	25	7.2	-	12(1)	G > A
	80	64.4/M	2/2	3	BD	Moderate	4	28.2	+	12(1)	G > T
	81	77.2/M	1/2	3	BD	Moderate	45	14.9	+		
	82	61.4/M	2/0	1	BD	Poor	90	17.7	-	12(1)	G > T
	83	53.5/F	4/0	3	BD	Moderate	23	29.4	-		
	84	50.6/F	2/0	1	BD	Moderate	57	78.5	-		
	85	60.2/M	1/0	1	BD/CC	Moderate	90	61.8	+		
	86	40.9/F	2/0	1	BD/PA	Moderate	15	83.7	-	12(2)	G > A

P-VALUES: Differentiation 0.01; Smoking 0.06; p53 0.99; K-ras 0.413; Stage 0.03; BA type 0.006

Note: Smoking=pack years; Survival=Months

Note: Classification: BD=Bronchial Derived; BA=Bronchioloalveolar; PA=Papillary; CC=Clear Cell; MU=Mucinous

* = Deceased

FIGURE 2A

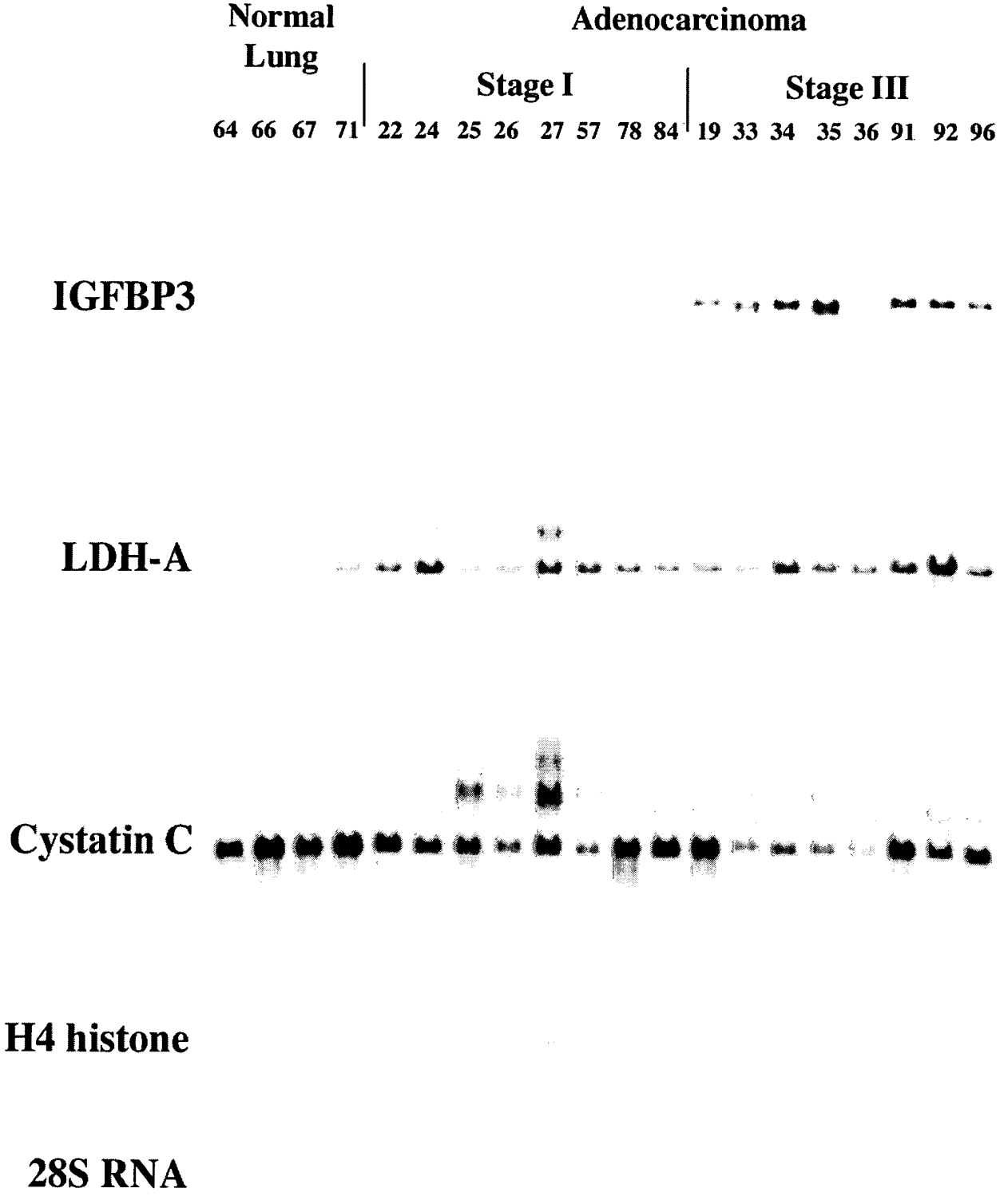

Normal Lung
Adenocarcinoma
Stage I
Stage III
64 66 67 71 22 24 25 26 27 57 78 84 19 33 34 35 36 91 92 96
IGFBP3
LDH-A
Cystatin C
H4 histone
28S RNA

Figure 2B

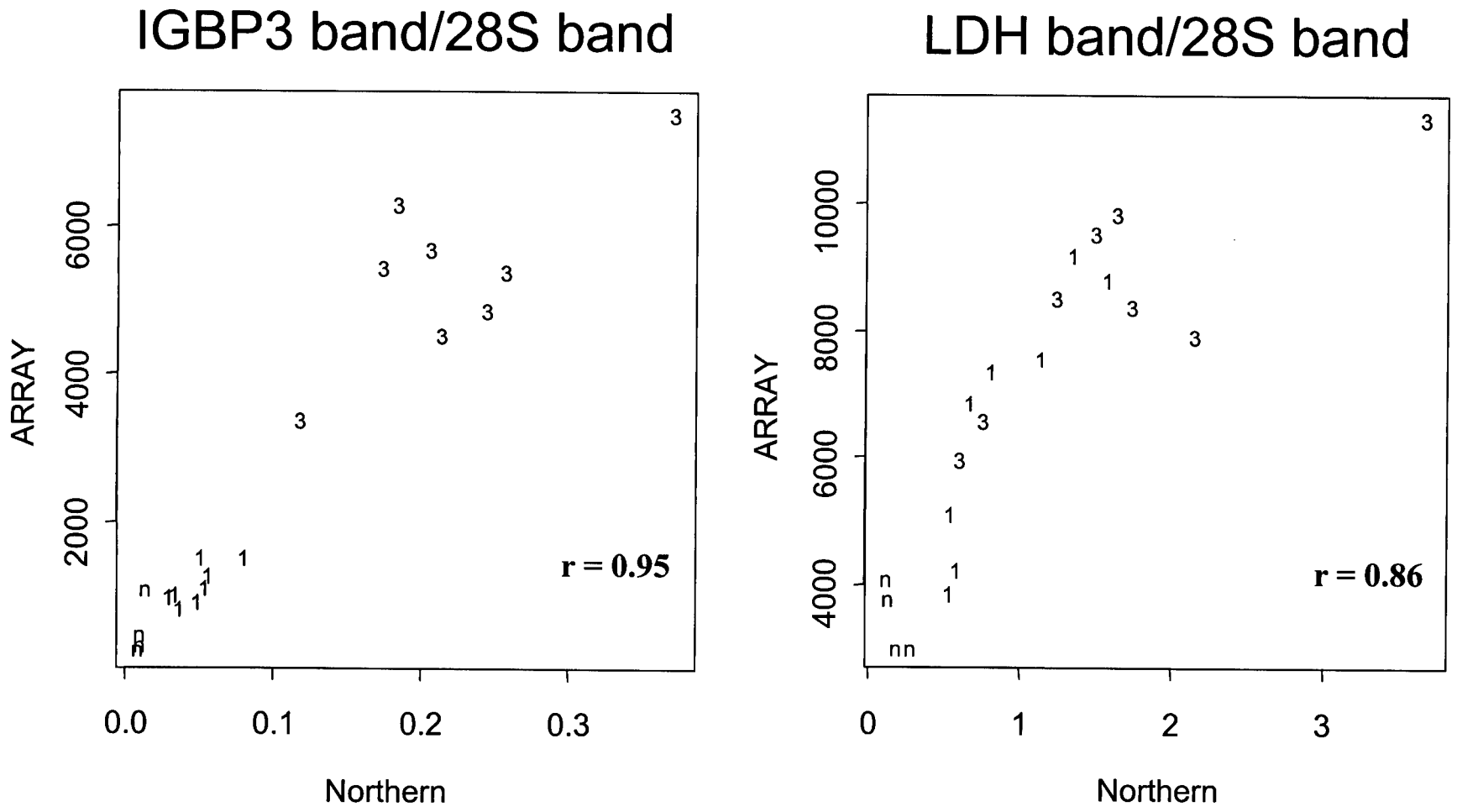
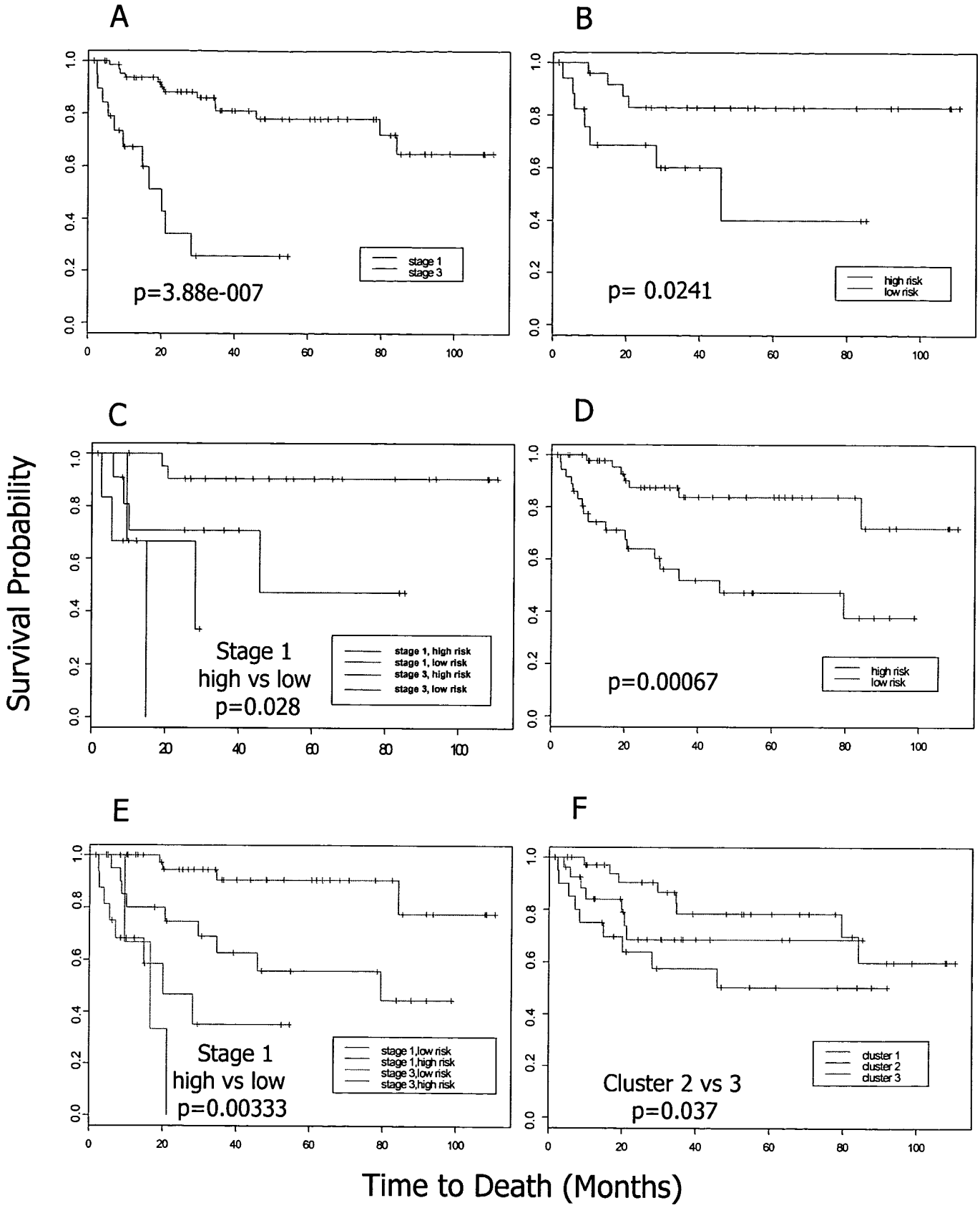

IGBP3 band/28S band
ARRAY
2000
4000
6000
0.0
0.1
0.2
0.3
Northern
r = 0.95
LDH band/28S band
ARRAY
4000
6000
8000
10000
0
1
2
3
Northern
r = 0.86

Figure 3


A
B
C
D
E
F
Survival Probability
Time to Death (Months)
p=3.88e-007
stage 1
stage 3
p= 0.0241
high risk
low risk
Stage 1
high vs low
p=0.028
stage 1, high risk
stage 1, low risk
stage 3, high risk
stage 3, low risk
p=0.00067
high risk
low risk
Stage 1
high vs low
p=0.00333
stage 1,low risk
stage 1,high risk
stage 3,low risk
stage 3,high risk
Cluster 2 vs 3
p=0.037
cluster 1
cluster 2
cluster 3

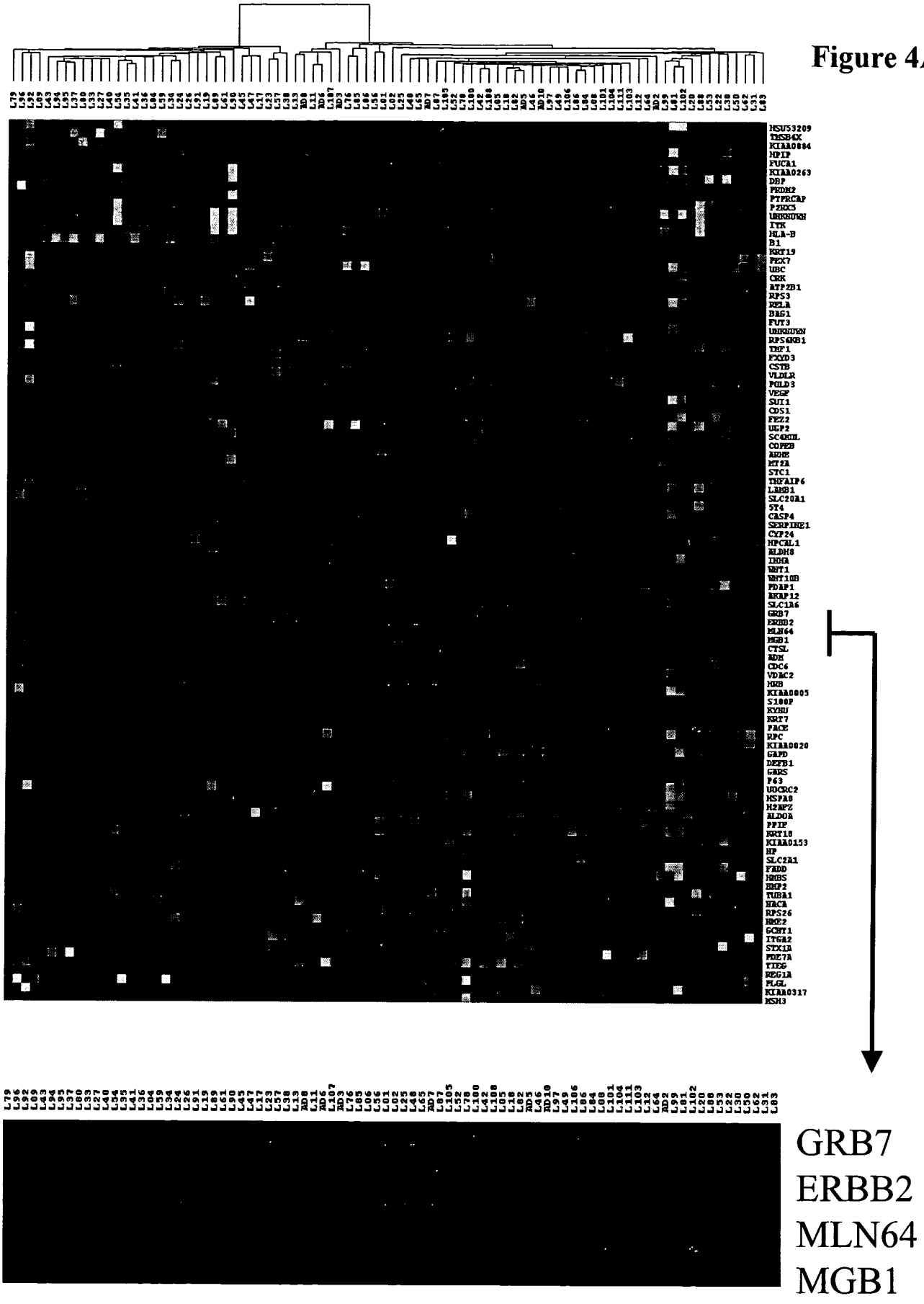


Figure 4A

Figure 4B

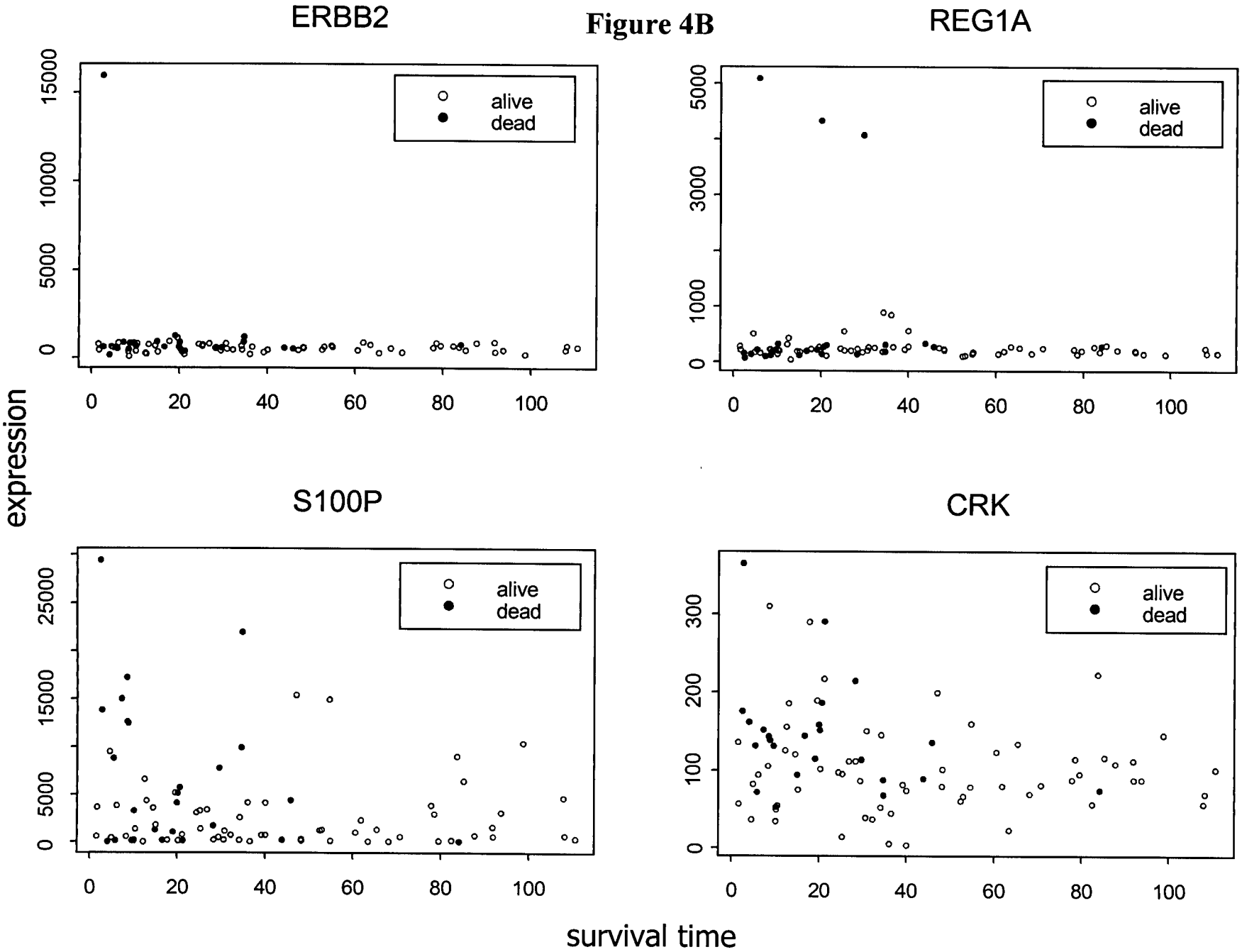

ERBB2
REG1A
S100P
CRK
alive
dead
expression
survival time
0
5000
10000
15000
1000
3000
25000
100
200
300
20
40
60
80
100

Figure 4C

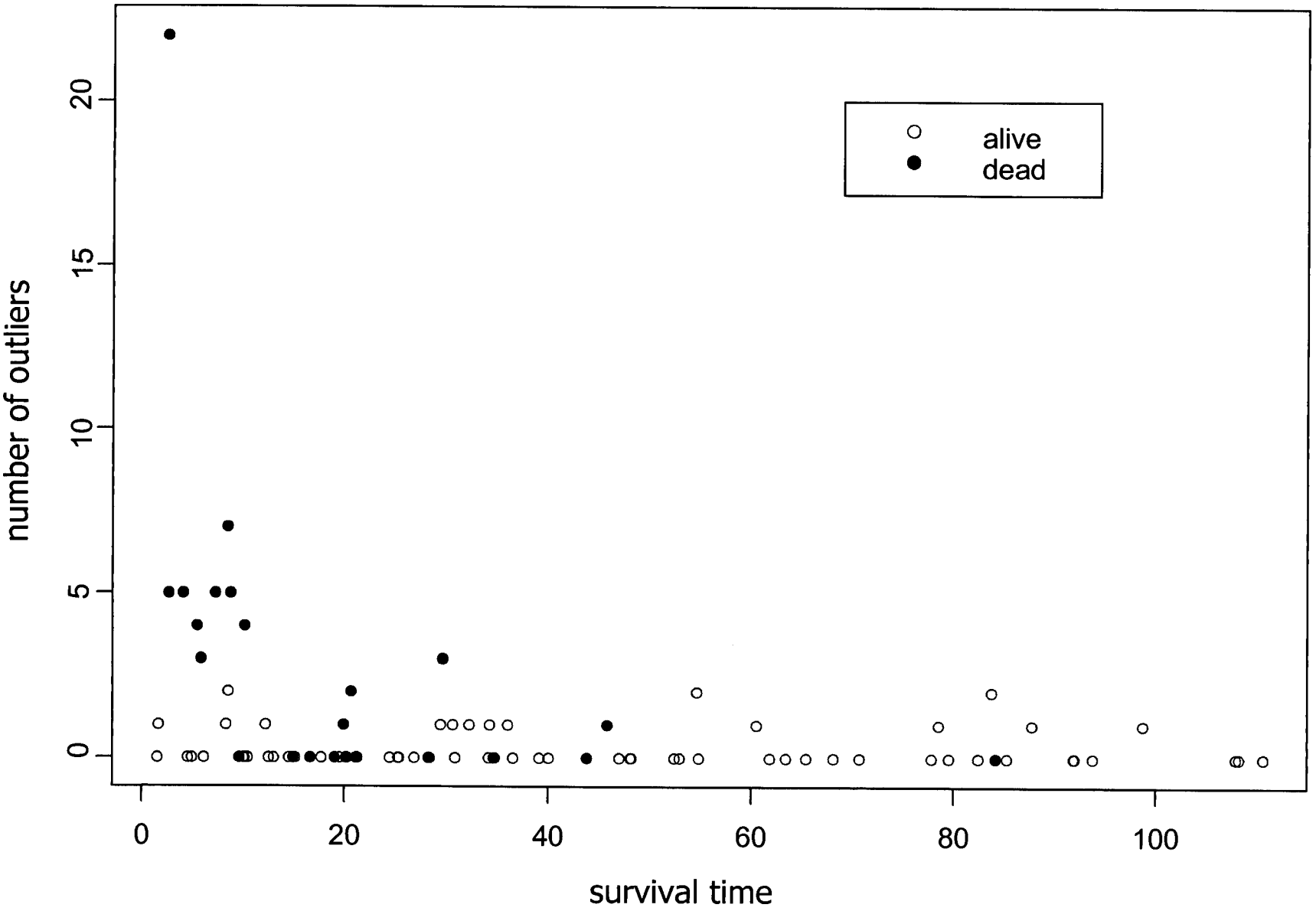

number of outliers
0
5
10
15
20
0
20
40
60
80
100
survival time
alive
dead

Figure 5

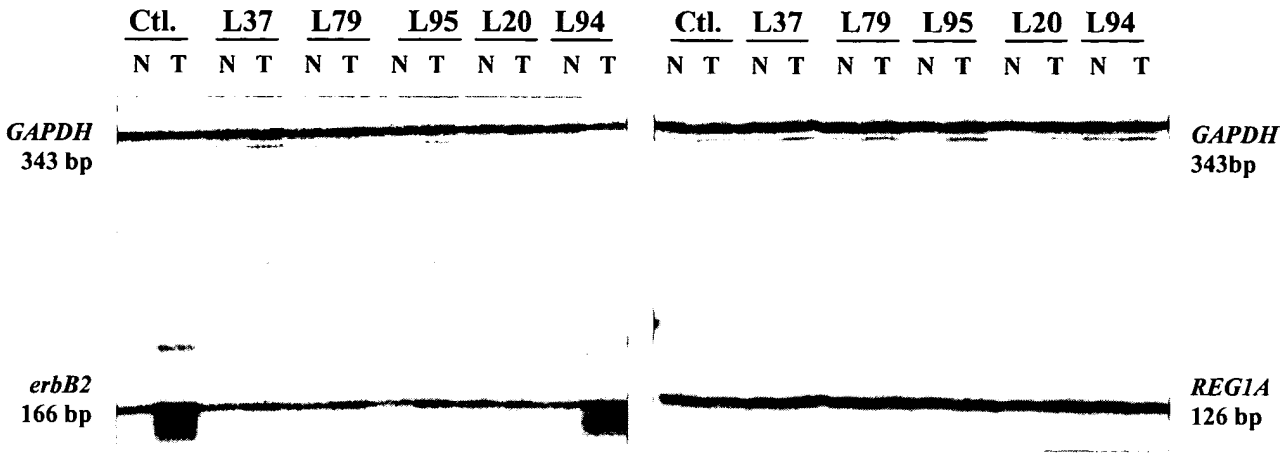

Ctl.
L37
L79
L95
L20
L94
N T N T N T N T N T N T
Ctl.
L37
L79
L95
L20
L94
N T N T N T N T N T N T
GAPDH
343 bp
GAPDH
343bp
erbB2
166 bp
REG1A
126 bp

Figure 6

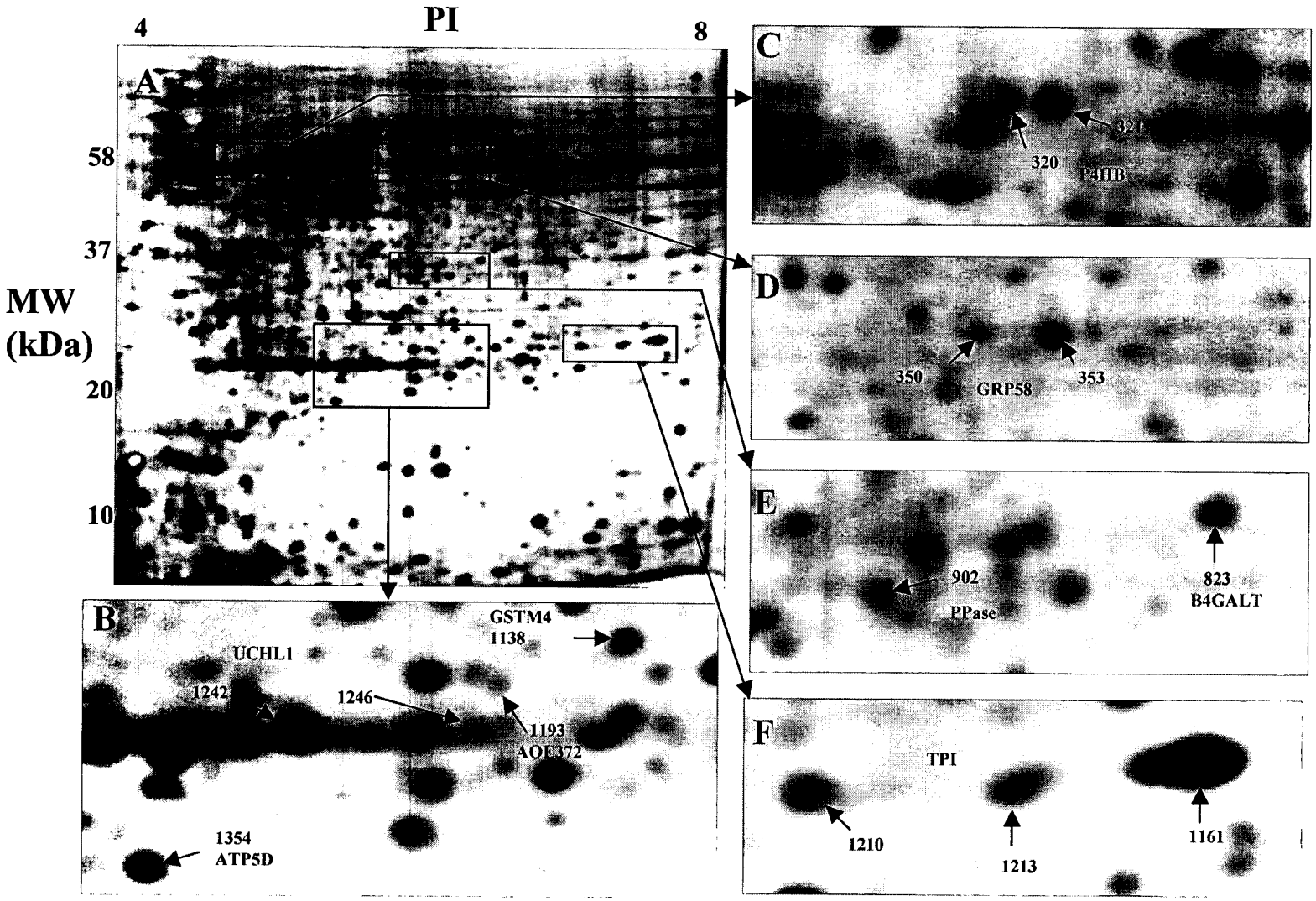

PI
4
8
A
58
37
20
10
MW
(kDa)
B
UCHL1
1242
1246
GSTM4
1138
1193
AOE372
1354
ATP5D
C
321
320
P4HB
D
350
GRP58
353
E
902
PPase
823
B4GALT
F
TPI
1210
1213
1161

Figure 7

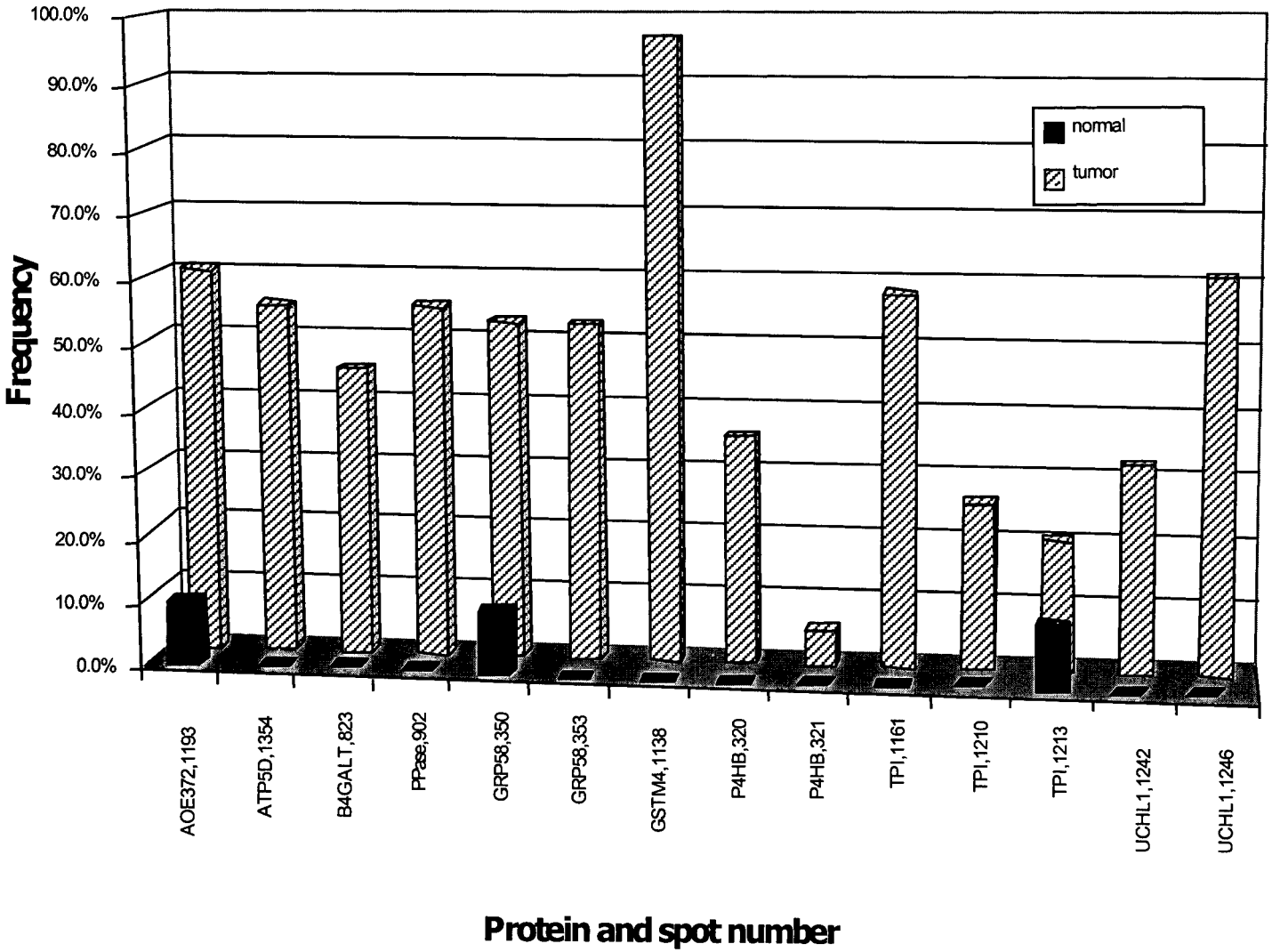

100.0%
90.0%
80.0%
70.0%
60.0%
50.0%
40.0%
30.0%
20.0%
10.0%
0.0%
Frequency
normal
tumor
AOE372,1193
ATP5D,1354
B4GALT,823
PPase,902
GRP58,350
GRP58,353
GSTM4,1138
P4HB,320
P4HB,321
TPI,1161
TPI,1210
TPI,1213
UCHL1,1242
UCHL1,1246
Protein and spot number

Figure 8

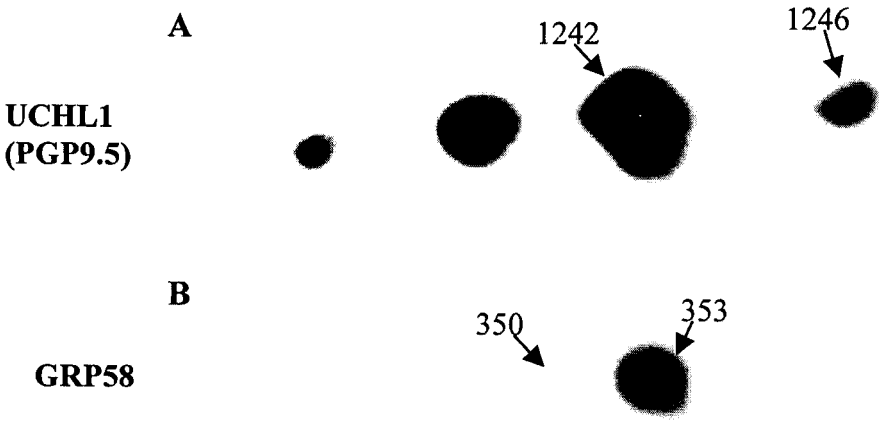


Figure 9

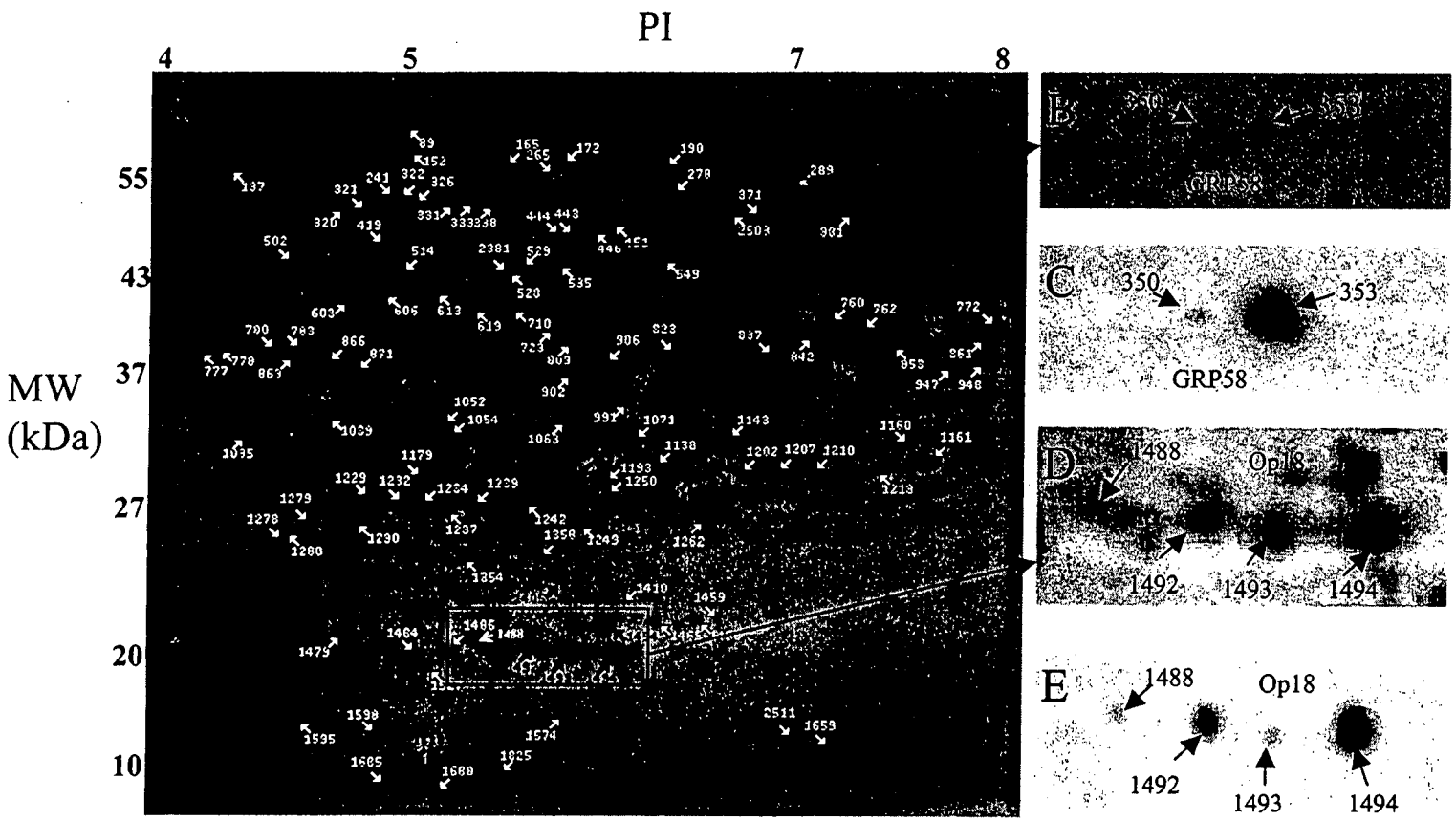

PI
4
5
7
8
MW
(kDa)
55
43
37
27
20
10
B
350
353
GRP58
C
350
353
GRP58
D
1488
Op18
1492
1493
1494
E
1488
Op18
1492
1493
1494

Figure 10

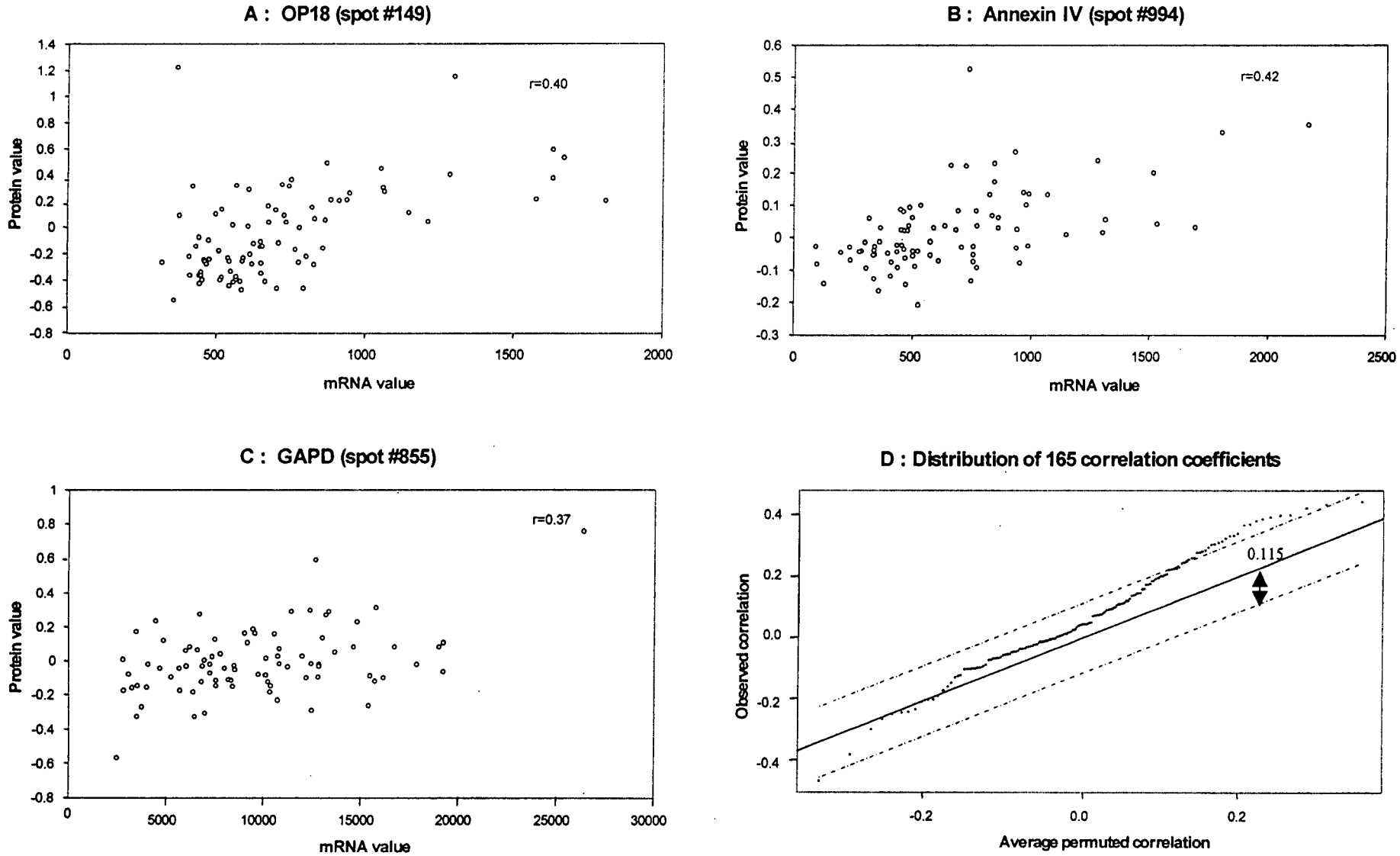
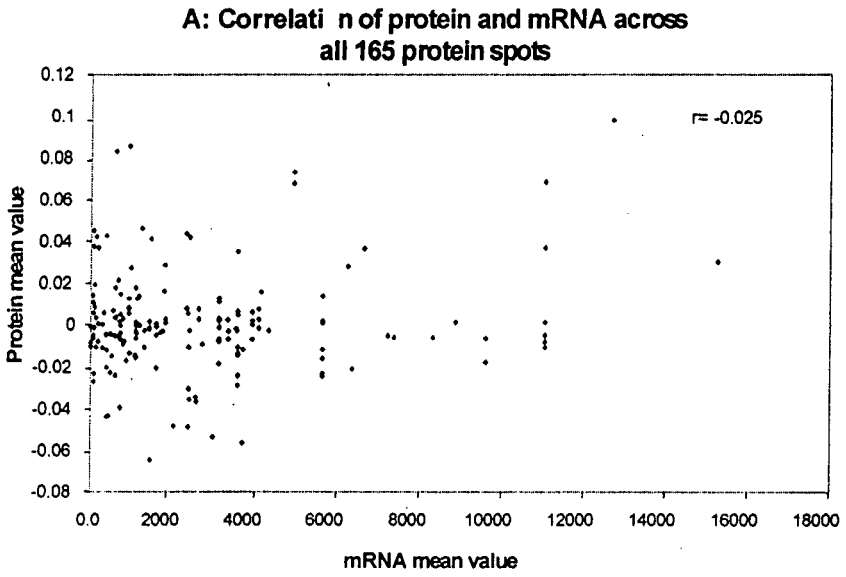
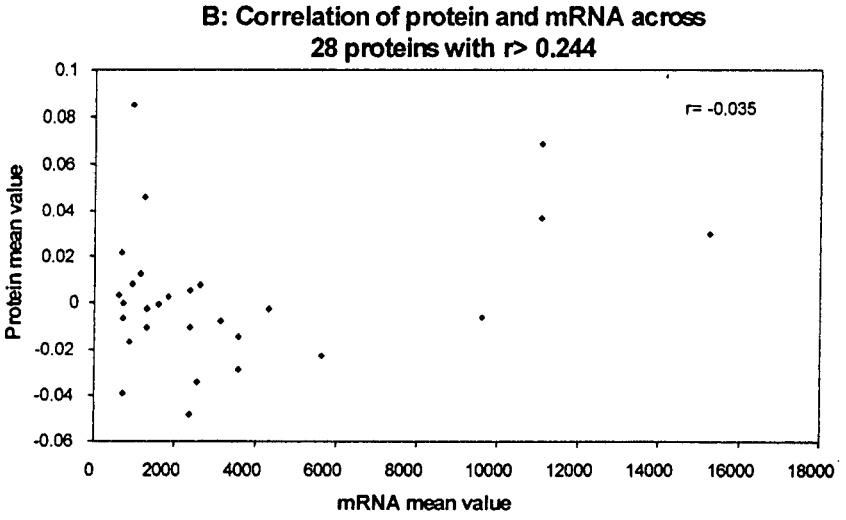

A : OP18 (spot #149)
r=0.40
Protein value
mRNA value
B : Annexin IV (spot #994)
r=0.42
Protein value
mRNA value
C : GAPD (spot #855)
r=0.37
Protein value
mRNA value
D : Distribution of 165 correlation coefficients
0.115
Observed correlation
Average permuted correlation

Figure 11


A: Correlati n of protein and mRNA across all 165 protein spots
r= -0.025
Protein mean value
mRNA mean value
0.12
0.1
0.08
0.06
0.04
0.02
0
-0.02
-0.04
-0.06
-0.08
0.0
2000
4000
6000
8000
10000
12000
14000
16000
18000


B: Correlation of protein and mRNA across 28 proteins with r> 0.244
r= -0.035
Protein mean value
mRNA mean value
0.1
0.08
0.06
0.04
0.02
0
-0.02
-0.04
-0.06
0
2000
4000
6000
8000
10000
12000
14000
16000
18000

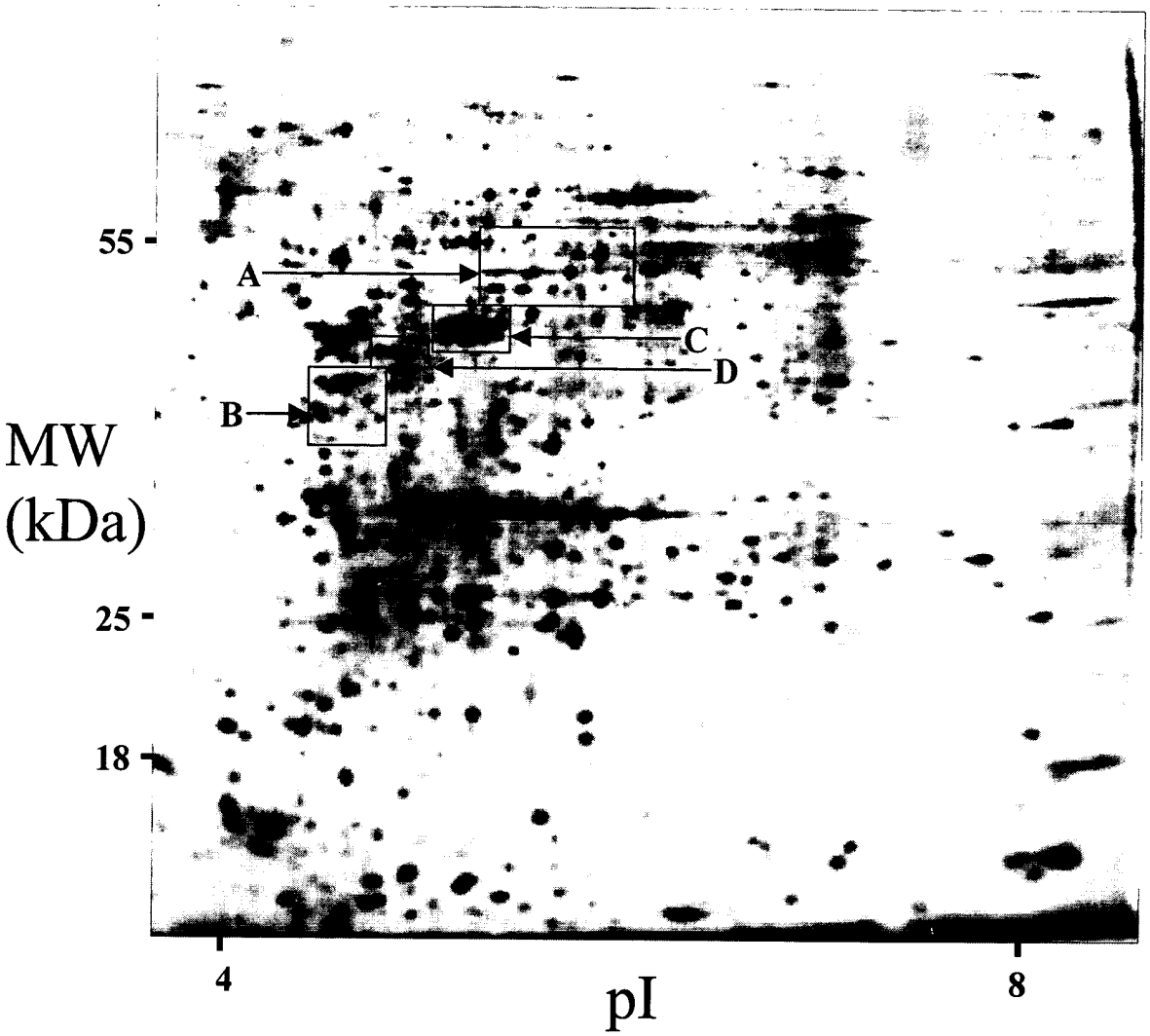


Figure 12

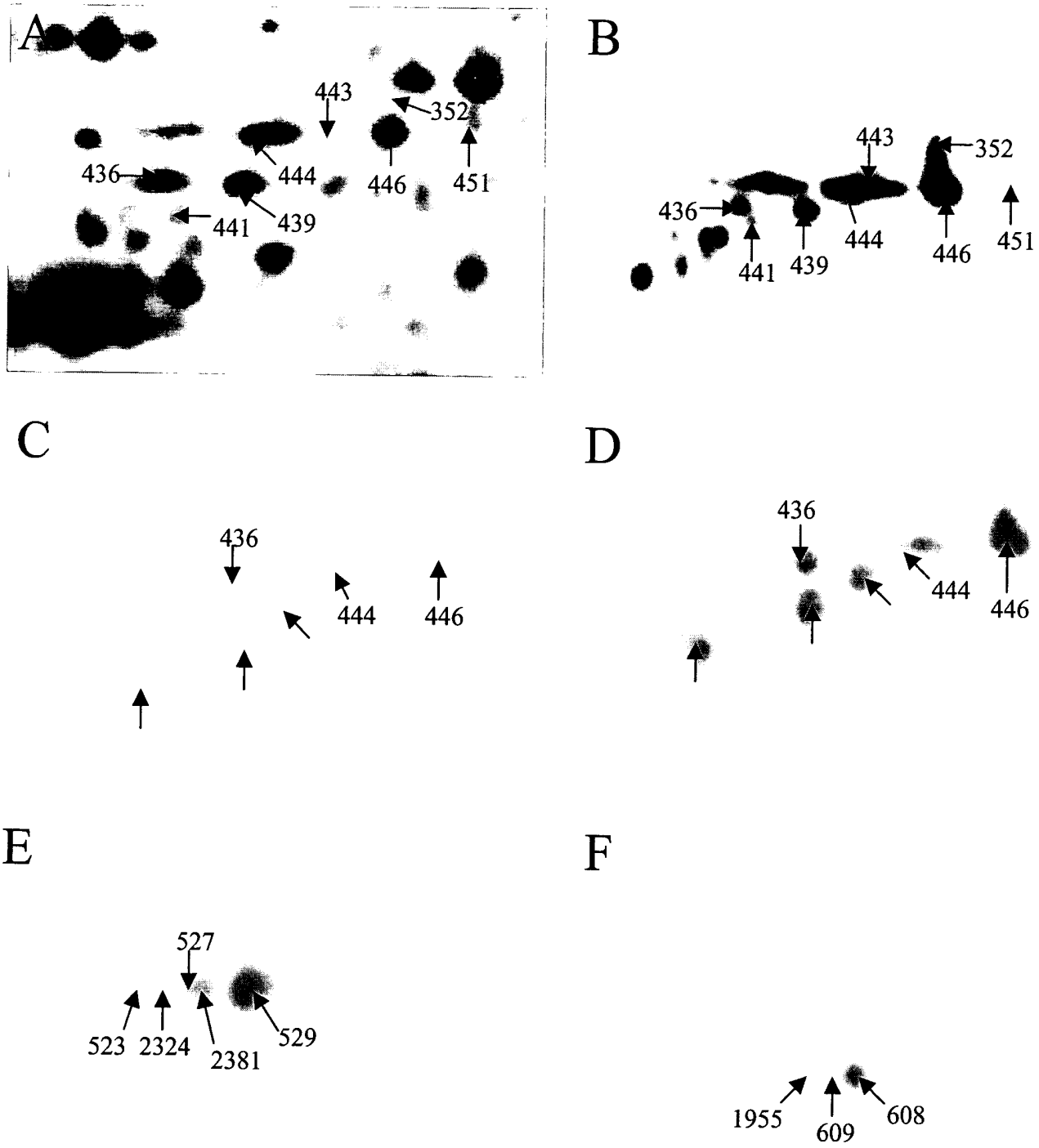

A
443
352
436
444
446
451
441
439
B
443
352
436
441
439
444
446
451
C
436
444
446
D
436
444
446
E
527
523
2324
2381
529
F
1955
609
608

Figure 3